

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Wang, Wei
Gish, Kurt C.
Schall, Thomas J.
Vicari, Alain P.
Zlotnik, Albert
- (ii) TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS
- (iii) NUMBER OF SEQUENCES: 19
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: DNAX Research Institute
 - (B) STREET: 901 California Avenue
 - (C) CITY: Palo Alto
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94304-1104
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/887,977
 - (B) FILING DATE: 03-JUL-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/021,644
 - (B) FILING DATE: 05-JUL-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/028,329
 - (B) FILING DATE: 11-OCT-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Ching, Edwin P.
 - (B) REGISTRATION NUMBER: 34,090
 - (C) REFERENCE/DOCKET NUMBER: DX0589K1
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 650-852-9192
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1034 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 94..525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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AGGCTACAAG CAGGCACCAG CTCTCAGGAC CAGAAAGGCA TTGGTGGCCC CCTTAAACCT      60
TCAGGTATCT GGAGAGGAGA TCTAACCTTC ACT ATG AAA CTG TGG CTT TTT GCC      114
                               Met Lys Leu Trp Leu Phe Ala
                               1           5
TGC CTG GTT GCC TGT TTT GTT GGG GCC TGG ATG CCG GTT GTC CAT GCC      162
Cys Leu Val Ala Cys Phe Val Gly Ala Trp Met Pro Val Val His Ala
          10           15           20
CAA GGT GCC TTT GAA GAC TGC TGC CTG GGT TAC CAG CAC AGG ATC AAA      210
Gln Gly Ala Phe Glu Asp Cys Cys Leu Gly Tyr Gln His Arg Ile Lys
          25           30           35
TGG AAT GTT CTC CGG CAT GCT AGG AAT TAT CAC CAG CAG GAA GTG AGT      258
Trp Asn Val Leu Arg His Ala Arg Asn Tyr His Gln Gln Glu Val Ser
          40           45           50           55
GGA AGC TGC AAC CTA CGT GCT GTG AGA TTC TAC TTC CGC CAG AAA GTA      306
Gly Ser Cys Asn Leu Arg Ala Val Arg Phe Tyr Phe Arg Gln Lys Val
          60           65           70
GTG TGT GGG AAT CCA GAG GAC ATG AAT GTG AAG AGG GCG ATA AGA ATC      354
Val Cys Gly Asn Pro Glu Asp Met Asn Val Lys Arg Ala Ile Arg Ile
          75           80           85
TTG ACA GCT AGG AAA AGG CTA GTC CAC TGG AAG AGC GCC TCA GAC TCT      402
Leu Thr Ala Arg Lys Arg Leu Val His Trp Lys Ser Ala Ser Asp Ser
          90           95           100
CAG ACT GAA AGG AAG AAG TCA AAC CAT ATG AAG TCC AAG GTG GAG AAC      450
Gln Thr Glu Arg Lys Lys Ser Asn His Met Lys Ser Lys Val Glu Asn
          105           110           115
CCC AAC AGT ACA AGC GTG AGG AGT GCC ACC CTA GGT CAT CCC AGG ATG      498
Pro Asn Ser Thr Ser Val Arg Ser Ala Thr Leu Gly His Pro Arg Met
          120           125           130           135
GTG ATG ATG CCC AGA AAG ACC AAC AAT TAAGTTAATT ACTCAGAGTA      545
Val Met Met Pro Arg Lys Thr Asn Asn
          140
AGCACCAGCT GGAGGATGGG CGGAGTCTGC TGAAGTGCTG TCTTCTAGGC ATGCCAGTGC      605
CAATGAACTC ACTGAAGCTA CAGTTTCCTG TACAAGACCA GACCCACCAA CGTCTCAGCA      665
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TGTACGAGGA AGGAACTACT GCGCTAAAGG CCCTCCCCT CACCAAGGAG CTATTGGCTA	725
TTGATGATTG CTGAGGGAAG GGAGTAATTT TTTTCTCTT TCTGAAGTGT GACTTGAGTA	785
AATTGCCCCAT AGTTCAGTAT ATAATCCCCA ACCTGTGCTC AGGCAAGCAA CCCTAATTAA	845
ATGCAATAGC CACATACAAA AGAAGAGGAT ATGAATAGTT TGGTAGGAGG GGCTTGTTAG	905
GAAGAAGACA TTAACAGGAG AGAGAGGAGC GAGAGGATAG TGAGTGTGTG AGAGTGCCTG	965
CACGTGTGAA ATGGTCAAAG AATTAAAAAA TAAAACTTA AAAAGCTATT AAAAAGTAAA	1025
AAAAATAAA	1034

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 144 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Lys	Leu	Trp	Leu	Phe	Ala	Cys	Leu	Val	Ala	Cys	Phe	Val	Gly	Ala	1	5	10	15
Trp	Met	Pro	Val	Val	His	Ala	Gln	Gly	Ala	Phe	Glu	Asp	Cys	Cys	Leu	20	25	30	
Gly	Tyr	Gln	His	Arg	Ile	Lys	Trp	Asn	Val	Leu	Arg	His	Ala	Arg	Asn	35	40	45	
Tyr	His	Gln	Gln	Glu	Val	Ser	Gly	Ser	Cys	Asn	Leu	Arg	Ala	Val	Arg	50	55	60	
Phe	Tyr	Phe	Arg	Gln	Lys	Val	Val	Cys	Gly	Asn	Pro	Glu	Asp	Met	Asn	65	70	75	80
Val	Lys	Arg	Ala	Ile	Arg	Ile	Leu	Thr	Ala	Arg	Lys	Arg	Leu	Val	His	85	90	95	
Trp	Lys	Ser	Ala	Ser	Asp	Ser	Gln	Thr	Glu	Arg	Lys	Lys	Ser	Asn	His	100	105	110	
Met	Lys	Ser	Lys	Val	Glu	Asn	Pro	Asn	Ser	Thr	Ser	Val	Arg	Ser	Ala	115	120	125	
Thr	Leu	Gly	His	Pro	Arg	Met	Val	Met	Met	Pro	Arg	Lys	Thr	Asn	Asn	130	135	140	

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1012 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 117..566

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 186..566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCGACCCACG CGTCCGCTTG GCCTACAGCC CGGCGGGCAT CAGCTCCCTT GACCCAGTGG	60
ATATCGGTGG CCCC GTTATT CGTCCAGGTG CCCAGGGAGG AGGACCCGCC TGCAGC	116
ATG AAC CTG TGG CTC CTG GCC TGC CTG GTG GCC GGC TTC CTG GGA GCC Met Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly Ala -23 -20 -15 -10	164
TGG GCC CCC GCT GTC CAC ACC CAA GGT GTC TTT GAG GAC TGC TGC CTG Trp Ala Pro Ala Val His Thr Gln Gly Val Phe Glu Asp Cys Cys Leu -5 1 5	212
GCC TAC CAC TAC CCC ATT GGG TGG GCT GTG CTC CGG CGC GCC TGG ACT Ala Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr 10 15 20 25	260
TAC CGG ATC CAG GAG GTG AGC GGG AGC TGC AAT CTG CCT GCT GCG ATA Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile 30 35 40	308
TTC TAC CTC CCC AAG AGA CAC AGG AAG GTG TGT GGG AAC CCC AAA AGC Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser 45 50 55	356
AGG GAG GTG CAG AGA GCC ATG AAG CTC CTG GAT GCT CGA AAT AAG GTT Arg Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val 60 65 70	404
TTT GCA AAG CTC CAC CAC AAC ATG CAG ACC TTC CAA GCA GGC CCT CAT Phe Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His 75 80 85	452
GCT GTA AAG AAG TTG AGT TCT GGA AAC TCC AAG TTA TCA TCA TCC AAG Ala Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys 90 95 100 105	500
TTT AGC AAT CCC ATC AGC AGC AGC AAG AGG AAT GTC TCC CTC CTG ATA Phe Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile 110 115 120	548

TCA GCT AAT TCA GGA CTG TGAGCCGGCT CATTTCTGGG CTCCATCGGC 596
 Ser Ala Asn Ser Gly Leu
 125

ACAGGAGGGG CCGGATCTTT CTCCGATAAA ACCGTCGCCC TACAGACCCA GCTGTCCCCA 656

CGCCTCTGTC TTTTGGGTCA AGTCTTAATC CCTGCACCTG AGTTGGTCCT CCCTCTGCAC 716

CCCCACCACC TCCTGCCCCG CTGGCAACTG GAAAGAAGGA GTTGGCCTGA TTTTAACCTT 776

TTGCCGCTCC GGGGAACAGC ACAATCCTGG GCAGCCAGTG GCTCTTGTAG AGAAAACTTA 836

GGATACCTCT CTCACCTTCT GTTTCTTGCC GTCCACCCCG GGCCATGCCA GTGTGTCTCTC 896

TGGGTCCCCT CCAAAAATCT GGTCATTCAA GGATCCCCTC CCAAGGCTAT GCTTTTCTAT 956

AACTTTTAAA TAAACCTTGG GGGGTGAATG GAATAAAAAA AAAAAAAAAA AAAAAA 1012

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly Ala
 -23 -20 -15 -10

Trp Ala Pro Ala Val His Thr Gln Gly Val Phe Glu Asp Cys Cys Leu
 -5 1 5

Ala Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr
 10 15 20 25

Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile
 30 35 40

Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser
 45 50 55

Arg Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val
 60 65 70

Phe Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His
 75 80 85

Ala Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys
 90 95 100 105

Phe Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile
 110 115 120

Ser Ala Asn Ser Gly Leu

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..288

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 79..288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG TGC TGT ACC AAG AGT TTG CTC CTG GCT GCT TTG ATG TCA GTG CTG	48
Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu	
-26 -25 -20 -15	
CTA CTC CAC CTC TGC GGC GAA TCA GAA GCA GCA AGC AAC TTT GAC TGC	96
Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys	
-10 -5 1 5	
TGT CTT GGA TAC ACA GAC CGT ATT CTT CAT CCT AAA TTT ATT GTG GGC	144
Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly	
10 15 20	
TTC ACA CGG CAG CTG GCC AAT GAA GGC TGT GAC ATC AAT GCT ATC ATC	192
Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile	
25 30 35	
TTT CAC ACA AAG AAA AAG TTG TCT GTG TGC GCA AAT CCA AAA CAG ACT	240
Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr	
40 45 50	
TGG GTG AAA TAT ATT GTG CGT CTC CTC AGT AAA AAA GTC AAG AAC ATG	288
Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met	
55 60 65 70	
TAAAAACTGT GGCTTTTCTG GAATGGAATT GGACATAGCC CAAGAACAGA AAGAACCTTG	348
CTGGGGTTGG AGGTTTCACT TGCACATCAT GGAGGGTTTA GTGCTTATCT AATTTGTGCC	408
TCACTGGACT TGTCCAATTA ATGAAGTTGA TTCATATTGC ATCATAGTTT GCTTTGTTTA	468
AGCATCACAT TAAAGTTAAA CTGTATTTTA TGTTATTTAT AGCTGTAGGT TTTCTGTGTT	528
TAGCTATTTA ATACTAATTT TCCATAAGCT ATTTTGTTTT AGTGCAAAGT ATAAAATTAT	588

ATTTGGGGGG GAATAAGATT ATATGGACTT TTTTGCAAGC AACAAAGCTAT TTTTAAAAA 648
 AAACATATTTA ACATTCTTTT GTTTATATTG TTTTGTCTCC TAAATTGTTG TAATTGCATT 708
 ATAAAATAAG AAAAATATTA ATAAGACAAA TATTGAAAAT AAAGAAACAA AAAGTTAAAA 768
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA 801

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu
 -26 -25 -20 -15
 Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys
 -10 -5 1 5
 Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
 10 15 20
 Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
 25 30 35
 Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
 40 45 50
 Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met
 55 60 65 70

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 142..435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCACGAGCG GCACGAGCAT CACTCACACC TTGCATTTCa CCCCTGCATC CCAGTCGCC 60

TGCAGCCTCA CACAGATCCT GCACACACCC AGACAGCTGG CGCTCACACA TTCACCGTTG	120
GCCTGCCTCT GTTCACCCTC C ATG GCC CTG CTA CTG GCC CTC AGC CTG CTG	171
Met Ala Leu Leu Leu Ala Leu Ser Leu Leu	
1 5 10	
GTT CTC TGG ACT TCC CCA GCC CCA ACT CTG AGT GGC ACC AAT GAT GCT	219
Val Leu Trp Thr Ser Pro Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala	
15 20 25	
GAA GAC TGC TGC CTG TCT GTG ACC CAG AAA CCC ATC CCT GGG TAC ATC	267
Glu Asp Cys Cys Leu Ser Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile	
30 35 40	
GTG AGG AAC TTC CAC TAC CTT CTC ATC AAG GAT GGC TGC AGG GTG CCT	315
Val Arg Asn Phe His Tyr Leu Leu Ile Lys Asp Gly Cys Arg Val Pro	
45 50 55	
GCT GTA GTG TTC ACC ACA CTG AGG GGC CGC CAG CTC TGT GCA CCC CCA	363
Ala Val Val Phe Thr Thr Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro	
60 65 70	
GAC CAG CCC TGG GTA GAA CGC ATC ATC CAG AGA CTG CAG AGG ACC TCA	411
Asp Gln Pro Trp Val Glu Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser	
75 80 85 90	
GCC AAG ATG AAG CGC CGC AGC AGT TAACCTATGA CCGTGCAGAG GGAGCCCGGA	465
Ala Lys Met Lys Arg Arg Ser Ser	
95	
GTCCGAGTCA AGCATTGTGA ATTATTACCT AACCTGGGGA ACCGAGGACC AGAAGGAAGG	525
ACCAGGCTTC CAGCTCCTCT GCACCAGACC TGACCAGCCA GGACAGGGCC TGGGGTGTGT	585
GTGAGTGTGA GTGTGAGCGA GAGGGTGAGT GTGGTCTAGA GTAAAGCTGC TCCACCCCCA	645
GATTGCAATG CTACCAATAA AGCCGCCTGG TGTTTACAAC TAAAAAAAAA AAAA	699

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Leu Leu Leu Ala Leu Ser Leu Leu Val Leu Trp Thr Ser Pro	
1 5 10 15	
Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala Glu Asp Cys Cys Leu Ser	
20 25 30	
Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile Val Arg Asn Phe His Tyr	

35 40 45
 Leu Leu Ile Lys Asp Gly Cys Arg Val Pro Ala Val Val Phe Thr Thr
 50 55 60
 Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro Asp Gln Pro Trp Val Glu
 65 70 75 80
 Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser Ala Lys Met Lys Arg Arg
 85 90 95
 Ser Ser

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG TTT TCG ACT CCA GTG AAG ATT ATT TTG TGT CAG TCA ATA CTT CAT	48
Met Phe Ser Thr Pro Val Lys Ile Ile Leu Cys Gln Ser Ile Leu His	
1 5 10 15	
ATT ACT CAG TTG ATT CTG AGA TGT TAC TGT GCT CCT TGC AGG AGG TCA	96
Ile Thr Gln Leu Ile Leu Arg Cys Tyr Cys Ala Pro Cys Arg Arg Ser	
20 25 30	
GGC AGT TCT CCA GGC TAT TTG TAC CGA ATT GCC TAC TCC TTG ATC TGT	144
Gly Ser Ser Pro Gly Tyr Leu Tyr Arg Ile Ala Tyr Ser Leu Ile Cys	
35 40 45	
GTT CTT GGC CTC CTG GGG AAT ATT CTG GTG GTG ATC ACC TTT GCT TTT	192
Val Leu Gly Leu Leu Gly Asn Ile Leu Val Val Ile Thr Phe Ala Phe	
50 55 60	
TAT AAG AAG GCC AGG TCT ATG ACA GAC GTC TAT CTC TTG AAC ATG GCC	240
Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala	
65 70 75 80	
ATT GCA GAC ATC CTC TTT GTT CTT ACT CTC CCA TTC TGG GCA GTG AGT	288
Ile Ala Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Ser	
85 90 95	
CAT GCC ACT GGT GCG TGG GTT TTC AGC AAT GCC ACG TGC AAG TTG CTA	336
His Ala Thr Gly Ala Trp Val Phe Ser Asn Ala Thr Cys Lys Leu Leu	

100										105					110					
AAA	GGC	ATC	TAT	GCC	ATC	AAC	TTT	AAC	TGC	GGG	ATG	CTG	CTC	CTG	ACT	384				
Lys	Gly	Ile	Tyr	Ala	Ile	Asn	Phe	Asn	Cys	Gly	Met	Leu	Leu	Leu	Thr					
		115				120						125								
TGC	ATT	AGC	ATG	GAC	CGG	TAC	ATC	GCC	ATT	GTA	CAG	GCG	ACT	AAG	TCA	432				
Cys	Ile	Ser	Met	Asp	Arg	Tyr	Ile	Ala	Ile	Val	Gln	Ala	Thr	Lys	Ser					
		130				135						140								
TTC	CGG	CTC	CGA	TCC	AGA	ACA	CTA	CCG	CGC	AGC	AAA	ATC	ATC	TGC	CTT	480				
Phe	Arg	Leu	Arg	Ser	Arg	Thr	Leu	Pro	Arg	Ser	Lys	Ile	Ile	Cys	Leu					
145				150						155				160						
GTT	GTG	TGG	GGG	CTG	TCA	GTC	ATC	ATC	TCC	AGC	TCA	ACT	TTT	GTC	TTC	528				
Val	Val	Trp	Gly	Leu	Ser	Val	Ile	Ile	Ser	Ser	Ser	Thr	Phe	Val	Phe					
				165				170						175						
AAC	CAA	AAA	TAC	AAC	ACC	CAA	GGC	AGC	GAT	GTC	TGT	GAA	CCC	AAG	TAC	576				
Asn	Gln	Lys	Tyr	Asn	Thr	Gln	Gly	Ser	Asp	Val	Cys	Glu	Pro	Lys	Tyr					
		180						185				190								
CAA	ACT	GTC	TCG	GAG	CCC	ATC	AGG	TGG	AAG	CTG	CTG	ATG	TTG	GGG	CTT	624				
Gln	Thr	Val	Ser	Glu	Pro	Ile	Arg	Trp	Lys	Leu	Leu	Met	Leu	Gly	Leu					
		195				200						205								
GAG	CTA	CTC	TTT	GGT	TTC	TTT	ATC	CCT	TTG	ATG	TTC	ATG	ATA	TTT	TGT	672				
Glu	Leu	Leu	Phe	Gly	Phe	Phe	Ile	Pro	Leu	Met	Phe	Met	Ile	Phe	Cys					
210				215						220										
TAC	ACG	TTC	ATT	GTC	AAA	ACC	TTG	GTG	CAA	GCT	CAG	AAT	TCT	AAA	AGG	720				
Tyr	Thr	Phe	Ile	Val	Lys	Thr	Leu	Val	Gln	Ala	Gln	Asn	Ser	Lys	Arg					
225				230						235				240						
CAC	AAA	GCC	ATC	CGT	GTA	ATC	ATA	GCT	GTG	GTG	CTT	GTG	TTT	CTG	GCT	768				
His	Lys	Ala	Ile	Arg	Val	Ile	Ile	Ala	Val	Val	Leu	Val	Phe	Leu	Ala					
				245				250						255						
TGT	CAG	ATT	CCT	CAT	AAC	ATG	GTC	CTG	CTT	GTG	ACG	GCT	GCT	AAT	TTG	816				
Cys	Gln	Ile	Pro	His	Asn	Met	Val	Leu	Leu	Val	Thr	Ala	Ala	Asn	Leu					
		260				265						270								
GGT	AAA	ATG	AAC	CGA	TCC	TGC	CAG	AGC	GAA	AAG	CTA	ATT	GGC	TAT	ACG	864				
Gly	Lys	Met	Asn	Arg	Ser	Cys	Gln	Ser	Glu	Lys	Leu	Ile	Gly	Tyr	Thr					
		275				280						285								
AAA	ACT	GTC	ACA	GAA	GTC	CTG	GCT	TTC	CTG	CAC	TGC	TGC	CTG	AAC	CCT	912				
Lys	Thr	Val	Thr	Glu	Val	Leu	Ala	Phe	Leu	His	Cys	Cys	Leu	Asn	Pro					
290				295						300										
GTG	CTC	TAC	GCT	TTT	ATT	GGG	CAG	AAG	TTC	AGA	AAC	TAC	TTT	CTG	AAG	960				
Val	Leu	Tyr	Ala	Phe	Ile	Gly	Gln	Lys	Phe	Arg	Asn	Tyr	Phe	Leu	Lys					
305				310						315				320						
ATC	TTG	AAG	GAC	CTG	TGG	TGT	GTG	AGA	AGG	AAG	TAC	AAG	TCC	TCA	GGC	1008				
Ile	Leu	Lys	Asp	Leu	Trp	Cys	Val	Arg	Arg	Lys	Tyr	Lys	Ser	Ser	Gly					
				325				330						335						

TTC TCC TGT GCC GGG AGG TAC TCA GAA AAC ATT TCT CGG CAG ACC AGT	1056
Phe Ser Cys Ala Gly Arg Tyr Ser Glu Asn Ile Ser Arg Gln Thr Ser	
340 345 350	
GAG ACC GCA GAT AAC GAC AAT GCG TCG TCC TTC ACT ATG TGATAGAAAG	1105
Glu Thr Ala Asp Asn Asp Asn Ala Ser Ser Phe Thr Met	
355 360 365	
CTGAGTCTCC CTAA	1119

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 365 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Phe Ser Thr Pro Val Lys Ile Ile Leu Cys Gln Ser Ile Leu His	
1 5 10 15	
Ile Thr Gln Leu Ile Leu Arg Cys Tyr Cys Ala Pro Cys Arg Arg Ser	
20 25 30	
Gly Ser Ser Pro Gly Tyr Leu Tyr Arg Ile Ala Tyr Ser Leu Ile Cys	
35 40 45	
Val Leu Gly Leu Leu Gly Asn Ile Leu Val Val Ile Thr Phe Ala Phe	
50 55 60	
Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala	
65 70 75 80	
Ile Ala Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Ser	
85 90 95	
His Ala Thr Gly Ala Trp Val Phe Ser Asn Ala Thr Cys Lys Leu Leu	
100 105 110	
Lys Gly Ile Tyr Ala Ile Asn Phe Asn Cys Gly Met Leu Leu Leu Thr	
115 120 125	
Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser	
130 135 140	
Phe Arg Leu Arg Ser Arg Thr Leu Pro Arg Ser Lys Ile Ile Cys Leu	
145 150 155 160	
Val Val Trp Gly Leu Ser Val Ile Ile Ser Ser Ser Thr Phe Val Phe	
165 170 175	
Asn Gln Lys Tyr Asn Thr Gln Gly Ser Asp Val Cys Glu Pro Lys Tyr	
180 185 190	

Gln	Thr	Val	Ser	Glu	Pro	Ile	Arg	Trp	Lys	Leu	Leu	Met	Leu	Gly	Leu
		195					200					205			
Glu	Leu	Leu	Phe	Gly	Phe	Phe	Ile	Pro	Leu	Met	Phe	Met	Ile	Phe	Cys
		210				215					220				
Tyr	Thr	Phe	Ile	Val	Lys	Thr	Leu	Val	Gln	Ala	Gln	Asn	Ser	Lys	Arg
		225			230					235					240
His	Lys	Ala	Ile	Arg	Val	Ile	Ile	Ala	Val	Val	Leu	Val	Phe	Leu	Ala
				245					250					255	
Cys	Gln	Ile	Pro	His	Asn	Met	Val	Leu	Leu	Val	Thr	Ala	Ala	Asn	Leu
			260					265					270		
Gly	Lys	Met	Asn	Arg	Ser	Cys	Gln	Ser	Glu	Lys	Leu	Ile	Gly	Tyr	Thr
		275					280					285			
Lys	Thr	Val	Thr	Glu	Val	Leu	Ala	Phe	Leu	His	Cys	Cys	Leu	Asn	Pro
		290				295					300				
Val	Leu	Tyr	Ala	Phe	Ile	Gly	Gln	Lys	Phe	Arg	Asn	Tyr	Phe	Leu	Lys
		305			310					315					320
Ile	Leu	Lys	Asp	Leu	Trp	Cys	Val	Arg	Arg	Lys	Tyr	Lys	Ser	Ser	Gly
				325					330					335	
Phe	Ser	Cys	Ala	Gly	Arg	Tyr	Ser	Glu	Asn	Ile	Ser	Arg	Gln	Thr	Ser
			340					345					350		
Glu	Thr	Ala	Asp	Asn	Asp	Asn	Ala	Ser	Ser	Phe	Thr	Met			
		355					360					365			

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1547 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 49..1116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGGAAGCTG CTTCGGGGGG TGAGCAAAC TTTTAAAATG CAGAAATT ATG ATC TAC
Met Ile Tyr
1

57

ACC	CGT	TTC	TTA	AAA	GGC	AGT	CTG	AAG	ATG	GCC	AAT	TAC	ACG	CTG	GCA
Thr	Arg	Phe	Leu	Lys	Gly	Ser	Leu	Lys	Met	Ala	Asn	Tyr	Thr	Leu	Ala
	5					10					15				

105

CCA GAG GAT GAA TAT GAT GTC CTC ATA GAA GGT GAA CTG GAG AGC GAT	153
Pro Glu Asp Glu Tyr Asp Val Leu Ile Glu Gly Glu Leu Glu Ser Asp	
20 25 30 35	
GAG GCA GAG CAA TGT GAC AAG TAT GAC GCC CAG GCA CTC TCA GCC CAG	201
Glu Ala Glu Gln Cys Asp Lys Tyr Asp Ala Gln Ala Leu Ser Ala Gln	
40 45 50	
CTG GTG CCA TCA CTC TGC TCT GCT GTG TTT GTG ATC GGT GTC CTG GAC	249
Leu Val Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly Val Leu Asp	
55 60 65	
AAT CTC CTG GTT GTG CTT ATC CTG GTA AAA TAT AAA GGA CTC AAA CGC	297
Asn Leu Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly Leu Lys Arg	
70 75 80	
GTG GAA AAT ATC TAT CTT CTA AAC TTG GCA GTT TCT AAC TTG TGT TTC	345
Val Glu Asn Ile Tyr Leu Leu Asn Leu Ala Val Ser Asn Leu Cys Phe	
85 90 95	
TTG CTT ACC CTG CCC TTC TGG GCT CAT GCT GGG GGC GAT CCC ATG TGT	393
Leu Leu Thr Leu Pro Phe Trp Ala His Ala Gly Gly Asp Pro Met Cys	
100 105 110 115	
AAA ATT CTC ATT GGA CTG TAC TTC GTG GGC CTG TAC AGT GAG ACA TTT	441
Lys Ile Leu Ile Gly Leu Tyr Phe Val Gly Leu Tyr Ser Glu Thr Phe	
120 125 130	
TTC AAT TGC CTT CTG ACT GTG CAA AGG TAC CTA GTG TTT TTG CAC AAG	489
Phe Asn Cys Leu Leu Thr Val Gln Arg Tyr Leu Val Phe Leu His Lys	
135 140 145	
GGC AAC TTT TTC TCA GCC AGG AGG AGG GTG CCC TGT GGC ATC ATT ACA	537
Gly Asn Phe Phe Ser Ala Arg Arg Arg Val Pro Cys Gly Ile Ile Thr	
150 155 160	
AGT GTC CTG GCA TGG GTA ACA GCC ATT CTG GCC ACT TTG CCT GAA TTC	585
Ser Val Leu Ala Trp Val Thr Ala Ile Leu Ala Thr Leu Pro Glu Phe	
165 170 175	
GTG GTT TAT AAA CCT CAG ATG GAA GAC CAG AAA TAC AAG TGT GCA TTT	633
Val Val Tyr Lys Pro Gln Met Glu Asp Gln Lys Tyr Lys Cys Ala Phe	
180 185 190 195	
AGC AGA ACT CCC TTC CTG CCA GCT GAT GAG ACA TTC TGG AAG CAT TTT	681
Ser Arg Thr Pro Phe Leu Pro Ala Asp Glu Thr Phe Trp Lys His Phe	
200 205 210	
CTG ACT TTA AAA ATG AAC ATT TCG GTT CTT GTC CTC CCC CTA TTT ATT	729
Leu Thr Leu Lys Met Asn Ile Ser Val Leu Val Leu Pro Leu Phe Ile	
215 220 225	
TTT ACA TTT CTC TAT GTG CAA ATG AGA AAA ACA CTA AGG TTC AGG GAG	777
Phe Thr Phe Leu Tyr Val Gln Met Arg Lys Thr Leu Arg Phe Arg Glu	
230 235 240	
CAG AGG TAT AGC CTT TTC AAG CTT GTT TTT GCC GTA ATG GTA GTC TTC	825

Gln	Arg	Tyr	Ser	Leu	Phe	Lys	Leu	Val	Phe	Ala	Val	Met	Val	Val	Phe	
245						250					255					
CTT	CTG	ATG	TGG	GCG	CCC	TAC	AAT	ATT	GCA	TTT	TTC	CTG	TCC	ACT	TTC	873
Leu	Leu	Met	Trp	Ala	Pro	Tyr	Asn	Ile	Ala	Phe	Phe	Leu	Ser	Thr	Phe	
260					265				270						275	
AAA	GAA	CAC	TTC	TCC	CTG	AGT	GAC	TGC	AAG	AGC	AGC	TAC	AAT	CTG	GAC	921
Lys	Glu	His	Phe	Ser	Leu	Ser	Asp	Cys	Lys	Ser	Ser	Tyr	Asn	Leu	Asp	
				280					285					290		
AAA	AGT	GTT	CAC	ATC	ACT	AAA	CTC	ATC	GCC	ACC	ACC	CAC	TGC	TGC	ATC	969
Lys	Ser	Val	His	Ile	Thr	Lys	Leu	Ile	Ala	Thr	Thr	His	Cys	Cys	Ile	
			295				300						305			
AAC	CCT	CTC	CTG	TAT	GCG	TTT	CTT	GAT	GGG	ACA	TTT	AGC	AAA	TAC	CTC	1017
Asn	Pro	Leu	Leu	Tyr	Ala	Phe	Leu	Asp	Gly	Thr	Phe	Ser	Lys	Tyr	Leu	
		310					315					320				
TGC	CGC	TGT	TTC	CAT	CTG	CGT	AGT	AAC	ACC	CCA	CTT	CAA	CCC	AGG	GGG	1065
Cys	Arg	Cys	Phe	His	Leu	Arg	Ser	Asn	Thr	Pro	Leu	Gln	Pro	Arg	Gly	
	325					330					335					
CAG	TCT	GCA	CAA	GGC	ACA	TCG	AGG	GAA	GAA	CCT	GAC	CAT	TCC	ACC	GAA	1113
Gln	Ser	Ala	Gln	Gly	Thr	Ser	Arg	Glu	Glu	Pro	Asp	His	Ser	Thr	Glu	
340				345				350						355		
GTG	TAA	ACT	AGCA	TCC	ACCA	AAAT	GCA	AGA	AAGAA	TAA	CAT	GGA	TTT	CAT	CTT	1166
Val																
TCT	GC	ATT	TAT	TTC	AT	GT	TAAA	TTTT	CT	TAC	AC	ATT	GT	TAT	AC	1226
AAG	GG	GAG	AGG	TG	AG	CT	AACA	TTT	GCT	AAGC	ACT	GA	ATTT	TG	TCT	1286
TCT	TT	TAC	AAA	CG	TG	AG	CTCC	TT	CG	CCT	CCT	AC	CA	TT	GT	1346
TCT	CA	TTT	TCT	CT	GAG	AAG	AA	ACT	AAG	GCG	CG	GAA	ATTT	TG	TCT	1406
AAG	TG	GC	CAG	ACT	GAT	TCT	CAG	CC	CT	TGGT	AG	CAT	TT	TG	CT	1466
GA	AC	AT	CA	AAA	CT	CA	AA	CCC	TG	GG	GAC	AA	CG	AT	GAA	1526
TAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	1547

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ile Tyr Thr Arg Phe Leu Lys Gly Ser Leu Lys Met Ala Asn Tyr

1	5	10	15
Thr	Leu	Ala	Pro
	20	Glu	Asp
		Glu	Tyr
		Asp	Val
		25	Leu
			Ile
			Glu
			Gly
			30
			Glu
			Leu
Glu	Ser	Asp	Glu
	35	Ala	Glu
		Gln	Cys
		40	Asp
		Lys	Tyr
			Asp
			45
			Ala
			Gln
			Ala
			Leu
Ser	Ala	Gln	Leu
	50	Val	Pro
		Ser	Leu
		55	Cys
		Ser	Ala
			Val
			60
			Phe
			Val
			Ile
			Gly
Val	Leu	Asp	Asn
	65	Leu	Leu
		70	Val
		Val	Val
		Leu	Ile
		Leu	Leu
		75	Val
			Lys
			Tyr
			Lys
			Gly
			80
Leu	Lys	Arg	Val
		85	Glu
		Asn	Ile
		Tyr	Leu
			Leu
			90
			Asn
			Leu
			Ala
			Val
			95
			Ser
			Asn
Leu	Cys	Phe	Leu
		100	Leu
		Thr	Leu
			Pro
			Phe
			105
			Trp
			Ala
			His
			Ala
			Gly
			110
			Gly
			Asp
Pro	Met	Cys	Lys
		115	Ile
		Leu	Ile
		Gly	Leu
		120	Tyr
		Phe	Val
			Gly
			125
			Leu
			Tyr
			Ser
Glu	Thr	Phe	Phe
	130	Asn	Cys
		Leu	Leu
		135	Thr
		Val	Gln
			Arg
			140
			Tyr
			Leu
			Val
			Phe
Leu	His	Lys	Gly
	145	Asn	Phe
		150	Phe
		Ser	Ala
		Arg	Arg
			155
			Arg
			Val
			Pro
			Cys
			160
			Gly
Ile	Ile	Thr	Ser
		165	Val
		Leu	Ala
		Trp	Val
			170
			Thr
			Ala
			Ile
			Leu
			Ala
			175
			Thr
			Leu
Pro	Glu	Phe	Val
		180	Val
		Tyr	Lys
		Pro	Gln
			185
			Met
			Glu
			Asp
			Gln
			190
			Lys
			Tyr
			Lys
Cys	Ala	Phe	Ser
		195	Arg
		Thr	Pro
			Phe
			200
			Leu
			Pro
			Ala
			Asp
			205
			Glu
			Thr
			Phe
			Trp
Lys	His	Phe	Leu
	210	Thr	Leu
		Lys	Met
		215	Asn
		Ile	Ser
			220
			Val
			Leu
			Val
			Leu
			Pro
Leu	Phe	Ile	Phe
	225	Thr	Phe
		230	Leu
		Tyr	Val
		Gln	Met
			235
			Arg
			Lys
			Thr
			Leu
			Arg
			240
Phe	Arg	Glu	Gln
		245	Arg
		Tyr	Ser
		Leu	Phe
			250
		Lys	Leu
		Val	Phe
			Ala
			255
			Val
			Met
Val	Val	Phe	Leu
		260	Leu
		Met	Trp
		Ala	Pro
			265
		Tyr	Asn
		Ile	Ala
			270
			Phe
			Phe
			Leu
Ser	Thr	Phe	Lys
		275	Glu
		His	Phe
			280
		Ser	Leu
		Ser	Asp
			285
			Cys
			Lys
			Ser
			Ser
			Tyr
Asn	Leu	Asp	Lys
	290	Ser	Val
		His	Ile
			295
		Thr	Lys
		Leu	Ile
			300
			Ala
			Thr
			Thr
			His
Cys	Cys	Ile	Asn
	305	Pro	Leu
		Leu	Tyr
		Ala	Phe
			315
		Leu	Asp
		Gly	Thr
			Phe
			Ser
			320

Lys Tyr Leu Cys Arg Cys Phe His Leu Arg Ser Asn Thr Pro Leu Gln
 325 330 335

Pro Arg Gly Gln Ser Ala Gln Gly Thr Ser Arg Glu Glu Pro Asp His
 340 345 350

Ser Thr Glu Val
 355

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Glu	Thr	Pro	Asn	Thr	Thr	Glu	Asp	Tyr	Asp	Thr	Thr	Thr	Glu	Phe	1	5	10	15
Asp	Tyr	Gly	Asp	Ala	Thr	Pro	Cys	Gln	Lys	Val	Asn	Glu	Arg	Ala	Phe	20	25	30	
Gly	Ala	Gln	Leu	Leu	Pro	Pro	Leu	Tyr	Ser	Leu	Val	Phe	Val	Ile	Gly	35	40	45	
Leu	Val	Gly	Asn	Ile	Leu	Val	Val	Leu	Val	Leu	Val	Gln	Tyr	Lys	Arg	50	55	60	
Leu	Lys	Asn	Met	Thr	Ser	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp	65	70	75	80
Leu	Leu	Phe	Leu	Phe	Thr	Leu	Pro	Phe	Trp	Ile	Asp	Tyr	Lys	Leu	Lys	85	90	95	
Asp	Asp	Trp	Val	Phe	Gly	Asp	Ala	Met	Cys	Lys	Ile	Leu	Ser	Gly	Phe	100	105	110	
Tyr	Tyr	Thr	Gly	Leu	Tyr	Ser	Glu	Ile	Phe	Phe	Ile	Ile	Leu	Leu	Thr	115	120	125	
Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Ala	Val	Phe	Ala	Leu	Arg	Ala	130	135	140	
Arg	Thr	Val	Thr	Phe	Gly	Val	Ile	Thr	Ser	Ile	Ile	Ile	Trp	Ala	Leu	145	150	155	160
Ala	Ile	Leu	Ala	Ser	Met	Pro	Gly	Leu	Tyr	Phe	Ser	Lys	Thr	Gln	Trp	165	170	175	

Glu	Phe	Thr	His	His	Thr	Cys	Ser	Leu	His	Phe	Pro	His	Glu	Ser	Leu	180	185	190
Arg	Glu	Trp	Lys	Leu	Phe	Gln	Ala	Leu	Lys	Leu	Asn	Leu	Phe	Gly	Leu	195	200	205
Val	Leu	Pro	Leu	Leu	Val	Met	Ile	Ile	Cys	Tyr	Thr	Gly	Ile	Ile	Lys	210	215	220
Ile	Leu	Leu	Arg	Arg	Pro	Asn	Glu	Lys	Lys	Ser	Lys	Ala	Val	Arg	Leu	225	230	235
Ile	Phe	Val	Ile	Met	Ile	Ile	Phe	Phe	Leu	Phe	Trp	Thr	Pro	Tyr	Asn	245	250	255
Leu	Thr	Ile	Leu	Ile	Ser	Val	Phe	Gln	Asp	Phe	Leu	Phe	Thr	His	Glu	260	265	270
Cys	Glu	Gln	Ser	Arg	His	Leu	Asp	Leu	Ala	Val	Gln	Val	Thr	Glu	Val	275	280	285
Ile	Ala	Tyr	Thr	His	Cys	Cys	Val	Asn	Pro	Val	Ile	Tyr	Ala	Phe	Val	290	295	300
Gly	Glu	Arg	Phe	Arg	Lys	Tyr	Leu	Arg	Gln	Leu	Phe	His	Arg	Arg	Val	305	310	315
Ala	Val	His	Leu	Val	Lys	Trp	Leu	Pro	Phe	Leu	Ser	Val	Asp	Arg	Leu	325	330	335
Glu	Arg	Val	Ser	Ser	Thr	Ser	Pro	Ser	Thr	Gly	Glu	His	Glu	Leu	Ser	340	345	350
Ala	Gly	Phe														355		

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 374 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Leu	Ser	Thr	Ser	Arg	Ser	Arg	Phe	Ile	Arg	Asn	Thr	Asn	Glu	Ser	1	5	10	15
Gly	Glu	Glu	Val	Thr	Thr	Phe	Phe	Asp	Tyr	Asp	Tyr	Gly	Ala	Pro	Cys	20	25	30	
His	Lys	Phe	Asp	Val	Lys	Gln	Ile	Gly	Ala	Gln	Leu	Leu	Pro	Pro	Leu				

35					40					45					
Tyr	Ser	Leu	Val	Phe	Ile	Phe	Gly	Phe	Val	Gly	Asn	Met	Leu	Val	Val
50						55					60				
Leu	Ile	Leu	Ile	Asn	Cys	Lys	Lys	Leu	Lys	Cys	Leu	Thr	Asp	Ile	Tyr
65				70						75					80
Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp	Leu	Leu	Phe	Leu	Ile	Thr	Leu	Pro
				85					90					95	
Leu	Trp	Ala	His	Ser	Ala	Ala	Asn	Glu	Trp	Val	Phe	Gly	Asn	Ala	Met
			100					105					110		
Cys	Lys	Leu	Phe	Thr	Gly	Leu	Tyr	His	Ile	Gly	Tyr	Phe	Gly	Gly	Ile
		115					120					125			
Phe	Phe	Ile	Ile	Leu	Leu	Thr	Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His
	130					135					140				
Ala	Val	Phe	Ala	Leu	Lys	Ala	Arg	Thr	Val	Thr	Phe	Gly	Val	Val	Thr
145					150					155					160
Ser	Val	Ile	Thr	Trp	Leu	Val	Ala	Val	Phe	Ala	Ser	Val	Pro	Gly	Ile
				165					170					175	
Ile	Phe	Thr	Lys	Cys	Gln	Lys	Glu	Asp	Ser	Val	Tyr	Val	Cys	Gly	Pro
			180					185					190		
Tyr	Phe	Pro	Arg	Gly	Trp	Asn	Asn	Phe	His	Thr	Ile	Met	Arg	Asn	Ile
		195					200					205			
Leu	Gly	Leu	Val	Leu	Pro	Leu	Leu	Ile	Met	Val	Ile	Cys	Tyr	Ser	Gly
	210					215					220				
Ile	Leu	Lys	Thr	Leu	Leu	Arg	Cys	Arg	Asn	Glu	Lys	Lys	Arg	His	Arg
225					230					235					240
Ala	Val	Arg	Val	Ile	Phe	Thr	Ile	Met	Ile	Val	Tyr	Phe	Leu	Phe	Trp
				245					250					255	
Thr	Pro	Tyr	Asn	Ile	Val	Ile	Leu	Leu	Asn	Thr	Phe	Gln	Glu	Phe	Phe
			260					265					270		
Gly	Leu	Ser	Asn	Cys	Glu	Ser	Thr	Ser	Gln	Leu	Asp	Gln	Ala	Thr	Gln
		275					280					285			
Val	Thr	Glu	Thr	Leu	Gly	Met	Thr	His	Cys	Cys	Ile	Asn	Pro	Ile	Ile
	290					295					300				
Tyr	Ala	Phe	Val	Gly	Glu	Lys	Phe	Arg	Ser	Leu	Phe	His	Ile	Ala	Leu
305					310					315					320
Gly	Cys	Arg	Ile	Ala	Pro	Leu	Gln	Lys	Pro	Val	Cys	Gly	Gly	Pro	Gly
				325					330					335	
Val	Arg	Pro	Gly	Lys	Asn	Val	Lys	Val	Thr	Thr	Gln	Gly	Leu	Leu	Asp
			340					345					350		

Gly Arg Gly Lys Gly Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu
 355 360 365

Gln Asp Lys Glu Gly Ala
 370

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Thr	Thr	Ser	Leu	Asp	Thr	Val	Glu	Thr	Phe	Gly	Thr	Thr	Ser	Tyr	1	5	10	15
Tyr	Asp	Asp	Val	Gly	Leu	Leu	Cys	Glu	Lys	Ala	Asp	Thr	Arg	Ala	Leu	20	25	30	
Met	Ala	Gln	Phe	Val	Pro	Pro	Leu	Tyr	Ser	Leu	Val	Phe	Thr	Val	Gly	35	40	45	
Leu	Leu	Gly	Asn	Val	Val	Val	Val	Met	Ile	Leu	Ile	Lys	Tyr	Arg	Arg	50	55	60	
Leu	Arg	Ile	Met	Thr	Asn	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp	65	70	75	80
Leu	Leu	Phe	Leu	Val	Thr	Leu	Pro	Phe	Trp	Ile	His	Tyr	Val	Arg	Gly	85	90	95	
His	Asn	Trp	Val	Phe	Gly	His	Gly	Met	Cys	Lys	Leu	Leu	Ser	Gly	Phe	100	105	110	
Tyr	His	Thr	Gly	Leu	Tyr	Ser	Glu	Ile	Phe	Phe	Ile	Ile	Leu	Leu	Thr	115	120	125	
Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Ala	Val	Phe	Ala	Leu	Arg	Ala	130	135	140	
Arg	Thr	Val	Thr	Phe	Gly	Val	Ile	Thr	Ser	Ile	Val	Thr	Trp	Gly	Leu	145	150	155	160
Ala	Val	Leu	Ala	Ala	Leu	Pro	Glu	Phe	Ile	Phe	Tyr	Glu	Thr	Glu	Glu	165	170	175	
Leu	Phe	Glu	Glu	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Pro	Glu	Asp	Thr	Val	180	185	190	

Tyr Ser Trp Arg His Phe His Thr Leu Arg Met Thr Ile Phe Cys Leu
 195 200 205
 Val Leu Pro Leu Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile Lys
 210 215 220
 Thr Leu Leu Arg Cys Pro Ser Lys Lys Lys Tyr Lys Ala Ile Arg Leu
 225 230 235 240
 Ile Phe Val Ile Met Ala Val Phe Phe Ile Phe Trp Thr Pro Tyr Asn
 245 250 255
 Val Ala Ile Leu Leu Ser Ser Tyr Gln Ser Ile Leu Phe Gly Asn Asp
 260 265 270
 Cys Glu Arg Ser Lys His Leu Asp Leu Val Met Leu Val Thr Glu Val
 275 280 285
 Ile Ala Tyr Ser His Cys Cys Met Asn Pro Val Ile Tyr Ala Phe Val
 290 295 300
 Gly Glu Arg Phe Arg Lys Tyr Leu Arg His Phe Phe His Arg His Leu
 305 310 315 320
 Leu Met His Leu Gly Arg Tyr Ile Pro Phe Leu Pro Ser Glu Lys Leu
 325 330 335
 Glu Arg Thr Ser Ser Val Ser Pro Ser Thr Ala Glu Pro Glu Leu Ser
 340 345 350
 Ile Val Phe
 355

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile Tyr
 1 5 10 15
 Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu
 20 25 30
 Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu
 35 40 45
 Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val Leu

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAATGATCA GTCAACGGGG GAC

23

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAGCAAGCT TGCAACCTTA ACCA

24

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asp Tyr Lys Asp Asp Asp Asp Lys Leu
1 5